



REPLACEMENT SHEET
Application No. 10/506,406, filed 3/14/05
Inventors: Swiercz et al.

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GAATTCCTGCAGCTCAGCAGCCGCCGAGAGCAGGACGAACCGCCAATCGCAAGGCACC
1 -----+-----+-----+-----+-----+-----+ 60
CTTAAGGACGTCGAGTCGTCGGCGGCGGTCTCGTCCTGCTTGGCGGTTAGCGTTCGTGG

TCTGAGAACTTCAGGATGCAGATGTCTCCAGCCCTCACCTGCCTAGTCCTGGGCTGGCC
61 -----+-----+-----+-----+-----+-----+ 120
AGACTCTTGAAGTCCTACGTCTACAGAGGTGCGGAGTGGACGGATCAGGACCCGGACCGG
aa M Q M S P A L T C L V L G L A -
|Signal Peptide
CTTGTCTTTGGTGAAGGTCTGCTGTGCACCATCCCCATCCTACGTGGCCACCTGGCC
121 -----+-----+-----+-----+-----+-----+ 180
GAACAGAAACCACTTCCCAGACGACAGTGGTAGGGGTAGGATGCACCGGGTGGACCGG
aa L V F G E G S A |V H H P P S Y V A H L A 12
Start Mature Protein
TCAGACTTCGGGGTGAGGGTGTTTCAGCAGGTGGCGCAGGCTCCAAGGACCGCAACGTG
181 -----+-----+-----+-----+-----+-----+ 240
AGTCTGAAGCCCCACTCCACAAAGTCGTCCACCGCGTCCGGAGGTTCTTGCGGTTGCAC
aa S D F G V R V F Q Q V A Q A S K D R N V 32

GTTTTCTCACCTATGGGGTGGCCTCGGTGTTGGCCATGCTCCAGCTGACAACAGGAGGA
241 -----+-----+-----+-----+-----+-----+ 300
CAAAAGAGTGGGATACCCACCGGAGCCACAACCGGTACGAGGTCGACTGTTGTCCTCCT
aa V F S P Y G V A S V L A M L Q L T T G G 52

GAAACCCAGCAGCAGATTCAAGCAGCTATGGGATTCAAGATTGATGACAAGGGCATGGCC
301 -----+-----+-----+-----+-----+-----+ 360
CTTTGGGTCGTCGTCTAAGTTCGTCGATACCCTAAGTTCTAACTACTGTTCCCGTACCGG
aa E T Q Q Q I Q A A M G F K I D D K G M A 72

CCCGCCCTCCGGCATCTGTACAAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGC
361 -----+-----+-----+-----+-----+-----+ 420
GGGCGGGAGGCCGTAGACATGTTCTCGAGTACCCCGGTACCTTGTTCTACTCTAGTCG
aa P A L R H L Y K E L M G P W N K D E I S 92

ACCACAGACGCGATCTTCGTCCAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCCAC
421 -----+-----+-----+-----+-----+-----+ 480
TGGTGTCTGCGCTAGAAGCAGGTGCGCCTAGACTTCGACCAGGTCCCGAAGTACGGGGTG
aa T T D A I F V Q R D L K L V Q G F M P H 112

TTCTTCAGGCTGTTCCGGAGCACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCC
481 -----+-----+-----+-----+-----+-----+ 540
AAGAAGTCCGACAAGGCCTCGTGCCAGTTCGTTACCTGAAAAGTCTCCACCTCTCTCGG
aa F F R L F R S T V K Q V D F S E V E R A 132

FIG.1A

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AGATTCATCATCAATGACTGGGTGAAGACACACACAAAAGGTATGATCAGCAACTTGCTT
541 -----+-----+-----+-----+-----+-----+ 600
TCTAAGTAGTAGTTACTGACCCACTTCTGTGTGTGTTTTCCATACTAGTCGTTGAACGAA
aa R F I I N D W V K T H T K G M I S N L L 152

GGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGCTGGTGAATGCCCTCTACTTCAAC
601 -----+-----+-----+-----+-----+-----+ 660
CCCTTTCCTCGGCACCTGGTCGACTGTGCCGACCACGACCACTTACGGGAGATGAAGTTG
aa G K G A V D Q L T R L V L V N A L Y F N 172

GGCCAGTGGAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCGCTCTTCCACAAATCA
661 -----+-----+-----+-----+-----+-----+ 720
CCGGTCACCTTCTGAGGGAAGGGGCTGAGGTCTGTTGGTGGCGGCGGAGAAGGTGTTTAGT
aa G Q W K T P F P D S S T H R R L F H K S 192

GACGGCAGCACTGTCTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAG
721 -----+-----+-----+-----+-----+-----+ 780
CTGCCGTCGTGACAGAGACACGGGTACTACCGAGTCTGGTTGTTCAAGTTGATATGACTC
aa D G S T V S V P M M A Q T N K F N Y T E 212

TTCACCACGCCCCGATGGCCATTACTACGACATCCTGGAAGTGCCTACCCACGGGGACACC
781 -----+-----+-----+-----+-----+-----+ 840
AAGTGGTGC GGCTACCGGTAATGATGCTGTAGGACCTTGACGGGATGGTGCCCTGTGG
aa F T T P D G H Y Y D I L E L P Y H G D T 232

CTCAGCATGTTCAATTGCTGCCCTTATGAAAAAGAGGTGCCTCTCTCTGCCCTCACCAAC
841 -----+-----+-----+-----+-----+-----+ 900
GAGTCGTACAAGTAACGACGGGGAATACTTTTTCTCCACGGAGAGAGACGGGAGTGGTTG
aa L S M F I A A P Y E K E V P L S A L T N 252

ATTCTGAGTGCCCAGCTCATCAGCCACTGGAAAGGCAACATGACCAGGCTGCCCCGCCTC
901 -----+-----+-----+-----+-----+-----+ 960
TAAGACTCACGGGTCGAGTAGTCGGTGACCTTTCGTTGTACTGGTCCGACGGGGCGGAG
aa I L S A Q L I S H W K G N M T R L P R L 272

CTGGTTCTGCCAAGTTCTCCCTGGAGACTGAAGTCGACCTCAGGAAGCCCCTAGAGAAC
961 -----+-----+-----+-----+-----+-----+ 1020
GACCAAGACGGGTTCAAGAGGGACCTCTGACTTCAGCTGGAGTCCTTCGGGGATCTCTTG
aa L V L P K F S L E T E V D L R K P L E N 292

CTGGGAATGACCGACATGTTTCAGACAGTTTCAGGCTGACTTCACGAGTCTTTCAGACCAA
1021 -----+-----+-----+-----+-----+-----+ 1080
GACCTTACTGGCTGTACAAGTCTGTCAAAGTCCGACTGAAGTGCTCAGAAAGTCTGGTT
aa L G M T D M F R Q F Q A D F T S L S D Q 312

FIG.1B

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1081 GAGCCTCTCCACGTCGCGCAGGCGCTGCAGAAAGTGAAGATCGAGGTGAACGAGAGTGGC
-----+-----+-----+-----+-----+-----+ 1140
CTCGGAGAGGTGCAGCGCGTCCGCGACGTCTTTCACCTTAGCTCCACTTGCTCTCACCG
aa E P L H V A Q A L Q K V K I E V N E S G 332

1141 ACGGTGGCCTCCTCATCCACAGCTGTCTAGTCTCAGCCCGCATGGCCCCGAGGAGATC
-----+-----+-----+-----+-----+-----+ 1200
TGCCACCGGAGGAGTAGGTGTGACAGTATCAGAGTCGGGCGTACCGGGGGCTCCTCTAG
aa T V A S S S T A V I V S A R M A P E E I 352

1201 ATCATGGACAGACCCTTCCTCTTTGTGGTCCGGCACAACCCACAGGAACAGTCCTTTTC
-----+-----+-----+-----+-----+-----+ 1260
TAGTACCTGTCTGGGAAGGAGAAACACCAGGCCGTGTTGGGGTGTCTTGTGAGGAAAAG
aa I M D R P F L F V V R H N P T G T V L F 352

1261 ATGGGCCAAGTGATGGAACCCTGACCCTGGGGAAGACGCCTTCATCTGGGACAAAAGT
-----+-----+-----+-----+-----+-----+ 1320
TACCCGGTTCACCTACCTGGGACTGGGACCCCTTTCTGCGGAAGTAGACCCTGTTTGTAC
aa M G Q V M E P * 379

1321 GAGATGCATCGGGAAAGAAGAACTCCGAAGAAAAGAATTTTAGTGTTAATGACTCTTTC
-----+-----+-----+-----+-----+-----+ 1380
CTCTACGTAGCCCTTTCTTCTTTGAGGCTTCTTTCTTAAATCACAATTACTGAGAAAAG

1381 TGAAGGAAGAGAAGACATTTGCCTTTTGTAAAAGATGGTAAACCAGATCTGTCTCCAAG
-----+-----+-----+-----+-----+-----+ 1440
ACTTCCTTCTCTTCTGTAAACGGAAAACAATTTTCTACCATTGTTGCTAGACAGAGGTTTC

1441 ACCTTGGCCTCTCCTTGGAGGACCTTTAGGTCAAACCTCCCTAGTCTCCACCTGAGACCCT
-----+-----+-----+-----+-----+-----+ 1500
TGGAACCGGAGAGGAACCTCCTGGAAATCCAGTTTGAGGGATCAGAGGTGGACTCTGGGA

1501 GGGAGAGAAGTTTGAAGCACAACCTCCCTTAAGGTCTCAAACCAGACGGTGACGCCTGCG
-----+-----+-----+-----+-----+-----+ 1560
CCCTCTCTTCAAACCTTCGTGTTGAGGGAATTCCAGAGGTTTGGTCTGCCACTGCGGACGC

1561 GGACCATCTGGGGCACCTGCTTCCACCCGTCTCTCTGCCCACTCGGGTCTGCAGACCTGG
-----+-----+-----+-----+-----+-----+ 1620
CCTGGTAGACCCCGTGGACGAAGGTGGGCAGAGAGACGGGTGAGCCAGACGTCTGGACC

1621 TTCCCACTGAGGCCCTTTGCAGGATGGAACCTACGGGGCTTACAGGAGCTTTTGTGTGCCT
-----+-----+-----+-----+-----+-----+ 1680
AAGGGTGACTCCGGGAAACGTCTACCTTGATGCCCCGAATGTCTCGAAAACACACGGA

FIG.1C

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1681 GGTAGAACTATTTCTGTTCCAGTCACATTGCCATCACTCTTGTACTGCCTGCCACCGCG
-----+-----+-----+-----+-----+-----+ 1740
CCATCTTTGATAAAGACAAGGTCAGTGTAAACGGTAGTGAGAACATGACGGACGGTGGCGC

GAGGAGGCTGGTGACAGGCCAAAGGCCAGTGGAAGAAACACCCTTTCATCTCAGAGTCCA
1741 -----+-----+-----+-----+-----+-----+ 1800
CTCCTCCGACCACTGTCCGGTTTCCGGTCACCTTCTTTGTGGGAAAGTAGAGTCTCAGGT

CTGTGGCACTGGCCACCCCTCCCCAGTACAGGGGTGCTGCAGGTGGCAGAGTGAATGTCC
1801 -----+-----+-----+-----+-----+-----+ 1860
GACACCGTGACCGGTGGGGAGGGGTCATGTCCCACGACGTCCACCGTCTCACTTACAGG

CCCATCATGTGGCCCAACTCTCCTGGCCTGGCCATCTCCCTCCCAGAAACAGTGTGCAT
1861 -----+-----+-----+-----+-----+-----+ 1920
GGGTAGTACACCGGTTGAGAGGACCGGACCGGTAGAGGGAGGGGTCTTTGTACACGTA

GGGTTATTTTGGAGTGTAGGTGACTTGTTTACTCATTGAAGCAGATTTCTGCTTCCTTTT
1921 -----+-----+-----+-----+-----+-----+ 1980
CCCAATAAAACCTCACATCCACTGAACAAATGAGTAACTTCGTCTAAAGACGAAGGAAAA

ATTTTTATAGGAATAGAGGAAGAAATGTCAGATGCGTGCCAGCTCTTCACCCCCCAATC
1981 -----+-----+-----+-----+-----+-----+ 2040
TAAAAATATCCTTATCTCCTTCTTTACAGTCTACGCACGGGTCGAGAAGTGGGGGGTTAG

TCTTGGTGGGGAGGGGTGTACCTAAATATTTATCATATCCTTGCCCTTGAGTGCTTGTTA
2041 -----+-----+-----+-----+-----+-----+ 2100
AGAACCACCCCTCCCCACATGGATTTATAAATAGTATAGGAACGGGAACCTCACGAACAAT

GAGAGAAAGAGAACTACTAAGGAAAATAATATTATTTAAACTCGCTCCTAGTGTTTCTTT
2101 -----+-----+-----+-----+-----+-----+ 2160
CTCTCTTTCTCTTGATGATTCCTTTTATTATAATAAATTTGAGCGAGGATCACAAAGAAA

GTGGTCTGTGTCACCGTATCTCAGGAAGTCCAGCCACTTGACTGGCACACACCCCTCCGG
2161 -----+-----+-----+-----+-----+-----+ 2220
CACCAGACACAGTGGCATAGAGTCCTTCAGGTCGGTGAACCTGACCGTGTGTGGGGAGGCC

ACATCCAGCGTGACGGAGCCCACTGCCACCTTGTTGGCCGCCTGAGACCCTCGCGCCCC
2221 -----+-----+-----+-----+-----+-----+ 2280
TGTAGGTGCACTGCCTCGGGTGTGACGGTGGAACACCGGCGGACTCTGGGAGCGCGGGG

CCGCGCCCCCGCGCCCCCTCTTTTCCCCTTGATGGAAATTGACCATACAATTTATCCT
2281 -----+-----+-----+-----+-----+-----+ 2340
GGCGCGGGGGGCGCGGGGAGAAAAAGGGGAACCTTTAACTGGTATGTTAAAGTAGGA

FIG. 1D

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2341 CCTTCAGGGGATCAAAAGGACGGAGTGGGGGGACAGAGACTCAGATGAGGACAGAGTGGT
-----+-----+-----+-----+-----+-----+ 2400
GGAAGTCCCCTAGTTTTCTGCCTACCCCCCTGTCTCTGAGTCTACTCCTGTCTCACCA

2401 TTCCAATGTGTTCAATAGATTTAGGAGCAGAAATGCAAGGGGCTGCATGACCTACCAGGA
-----+-----+-----+-----+-----+-----+ 2460
AAGGTTACACAAGTTATCTAAATCCTCGTCTTTACGTTCCCCGACGTACTGGATGGTCCT

2461 CAGAACTTTCCCAATTACAGGGTGACTCACAGCCGATTGGTGACTCACTTCAATGTGT
-----+-----+-----+-----+-----+-----+ 2520
GTCTTGAAAGGGGTTAATGTCCCACTGAGTGTGCGCGTAACCACTGAGTGAAGTTACACA

2521 CATTTCCGGCTGCTGTGTGTGAGCAGTGGACACGTGAGGGGGGGTGGGTGAGAGAGACA
-----+-----+-----+-----+-----+-----+ 2580
GTAAAGGCCGACGACACACTCGTCACCTGTGCACTCCCCCCCCACCACTCTCTCTGT

2581 GGCAGCTCGGATTCAACTACCTTAGATAATATTTCTGAAAACCTACCAGCCAGAGGGTAG
-----+-----+-----+-----+-----+-----+ 2640
CCGTCGAGCCTAAGTTGATGGAATCTATTATAAAGACTTTTGGATGGTCGGTCTCCCATC

2641 GGCACAAAGATGGATGTAATGCACTTTGGGAGGCCAAGGCCGGGAGGATTGCTTGAGCCCA
-----+-----+-----+-----+-----+-----+ 2700
CCGTGTTTCTACCTACATTACGTGAAACCTCCGGTTCCGCCCTCCTAACGAACTCGGGT

2701 GGAGTTCAAGACCAGCCTGGGCAACATACCAAGACCCCCGTCTCTTTAAAAATATATATA
-----+-----+-----+-----+-----+-----+ 2760
CCTCAAGTTCTGGTCGGACCCGTTGTATGGTTCTGGGGCAGAGAAATTTTATATATAT

2761 TTTTAAATATACTTAAATATATATTTCTAATATCTTTAAATATATATATATATTTTAAAG
-----+-----+-----+-----+-----+-----+ 2820
AAAATTTATATGAATTTATATATAAAGATTATAGAAATTTATATATATATATAAAATTC

2821 ACCAATTTATGGGAGAATTGCACACAGATGTGAAATGAATGTAATCTAATAGAAGC
-----+-----+-----+-----+-----+-----+ 2876
TGGTTAAATACCCTCTTAACGTGTGTCTACACTTTACTTACATTAGATTATCTTCG
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FIG. 1E

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MQMSPALTCLVLGLALVFGEGSA
Signal Peptide

VHHPPSYVAHLASDFGVRVFQQVAQASKDRNVFSPYGVASVLAMLQLTTGGETQQQIQA
AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTDAIFVQRDLKLVGFMPPHFFRLFRST
VKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP
DSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLMSFIAAP
YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR
QFQADFTSLSDQEPLHVAQALQVKVIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFLF
VVRHNPTGTVLFMGQVMEP

FIG.2A

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10	20	30	40	50	60
VHHP	SYVA	HLAS	DFGVR	VFQQ	VAQAS
KDRN	VVFS	SPYGV	ASVL	AMLQ	LT
TTG	GET	QQQ	IQ		
70	80	90	100	110	120
AMGF	KIDD	KMAP	ALRH	LYKE	LMGP
WNKD	EIST	TD	AI	FVQR	DLKL
VQG	FMPH	FFRL	FRST		
130	140	150	160	170	180
VKQV	DFSE	VERA	RFI	INDW	KTH
KGM	ISN	LLGK	GA	VDQL	TRLV
LVN	ALY	FNGQ	WKT	PF	
190	200	210	220	230	240
DSST	HRRL	FKSD	GSTV	SVP	MAQT
NKF	NYTE	FTTP	DGH	YD	I
LELP	YHGD	TLSM	FIA	AP	
250	260	270	280	290	300
YEKE	VPLS	AL	TN	IL	SA
QL	IS	HW	KGN	MTR	LP
RL	LV	PK	FS	LE	TE
VD	LR	KP	LE	N	LG
MT	DM	FR			
310	320	330	340	350	360
QFQA	DFTS	LS	DQ	EL	H
VA	QAL	QK	V	KN	ES
GT	V	AS	S	T	A
V	I	S	A	R	M
A	P	E	E	I	I
M	D	R	P	F	L
F					
370					
VVRH	NPTG	TV	LF	MG	QV
MEP					

FIG.2B

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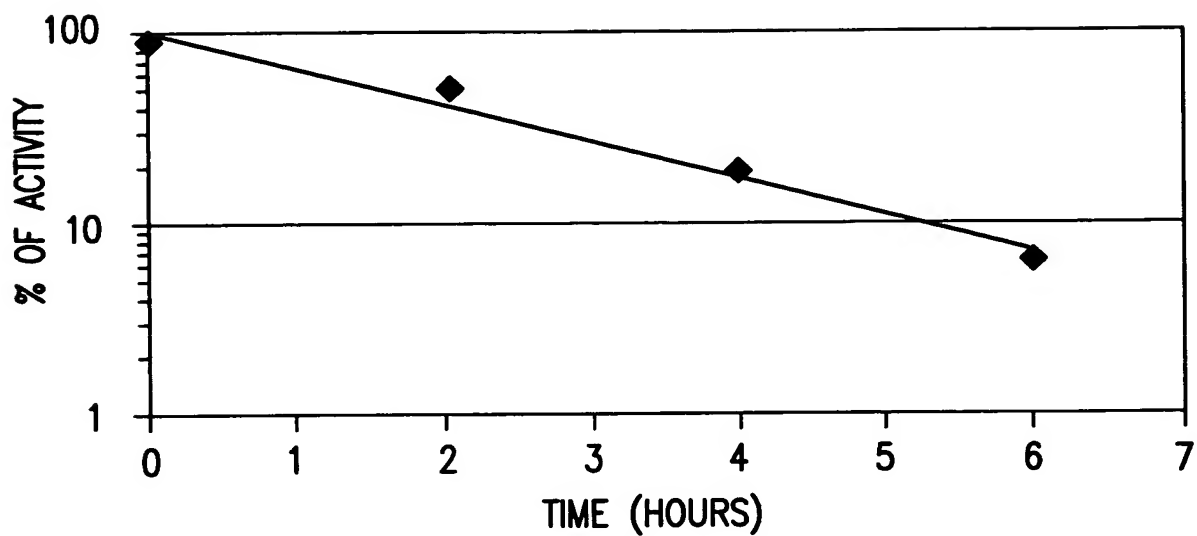


FIG.3

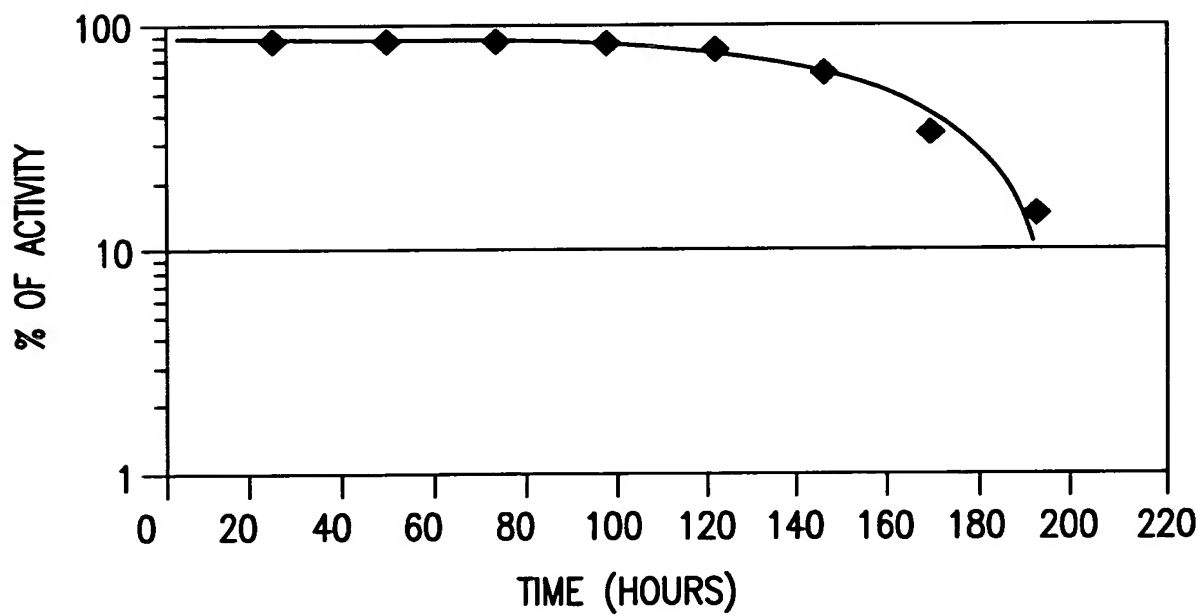


FIG.4

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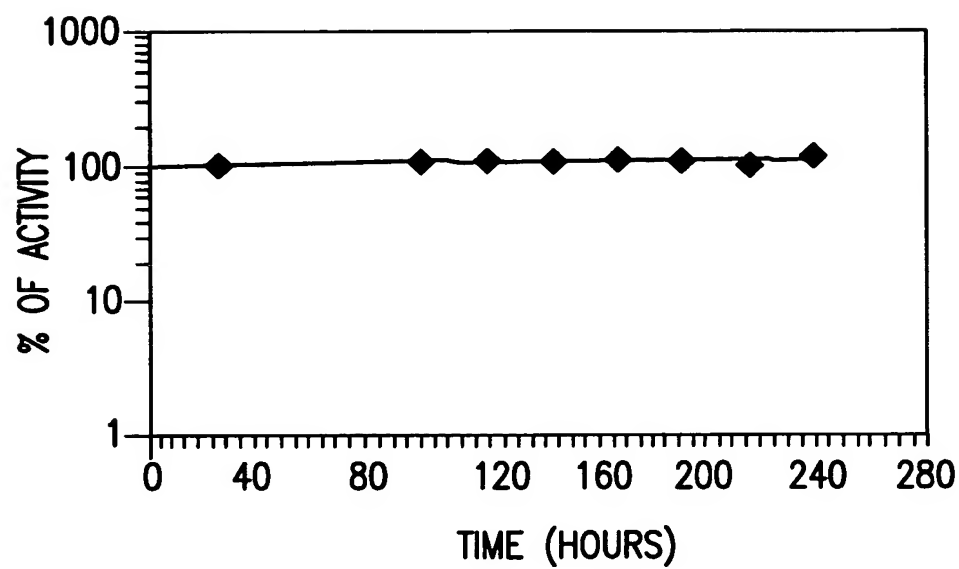


FIG.5

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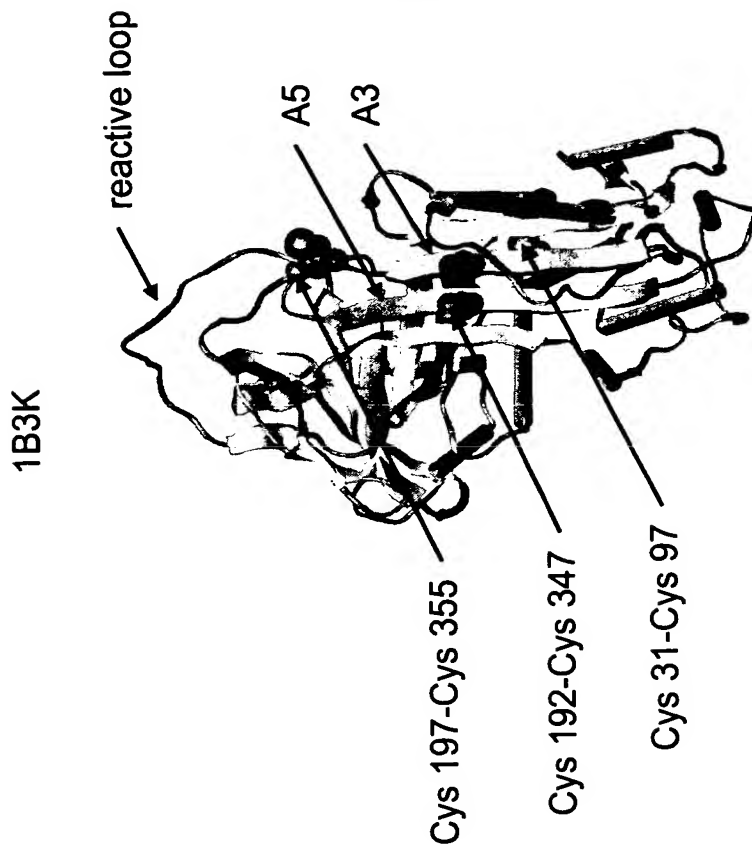


FIG. 6B

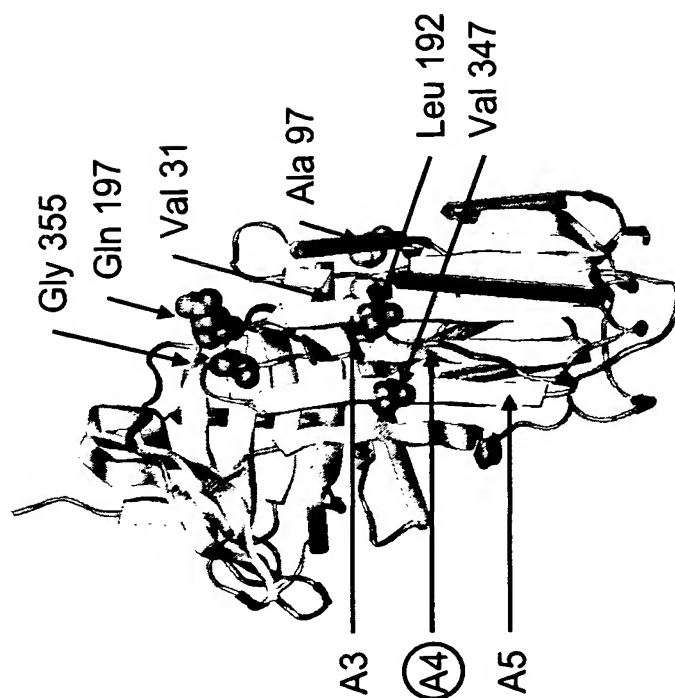


FIG. 6A

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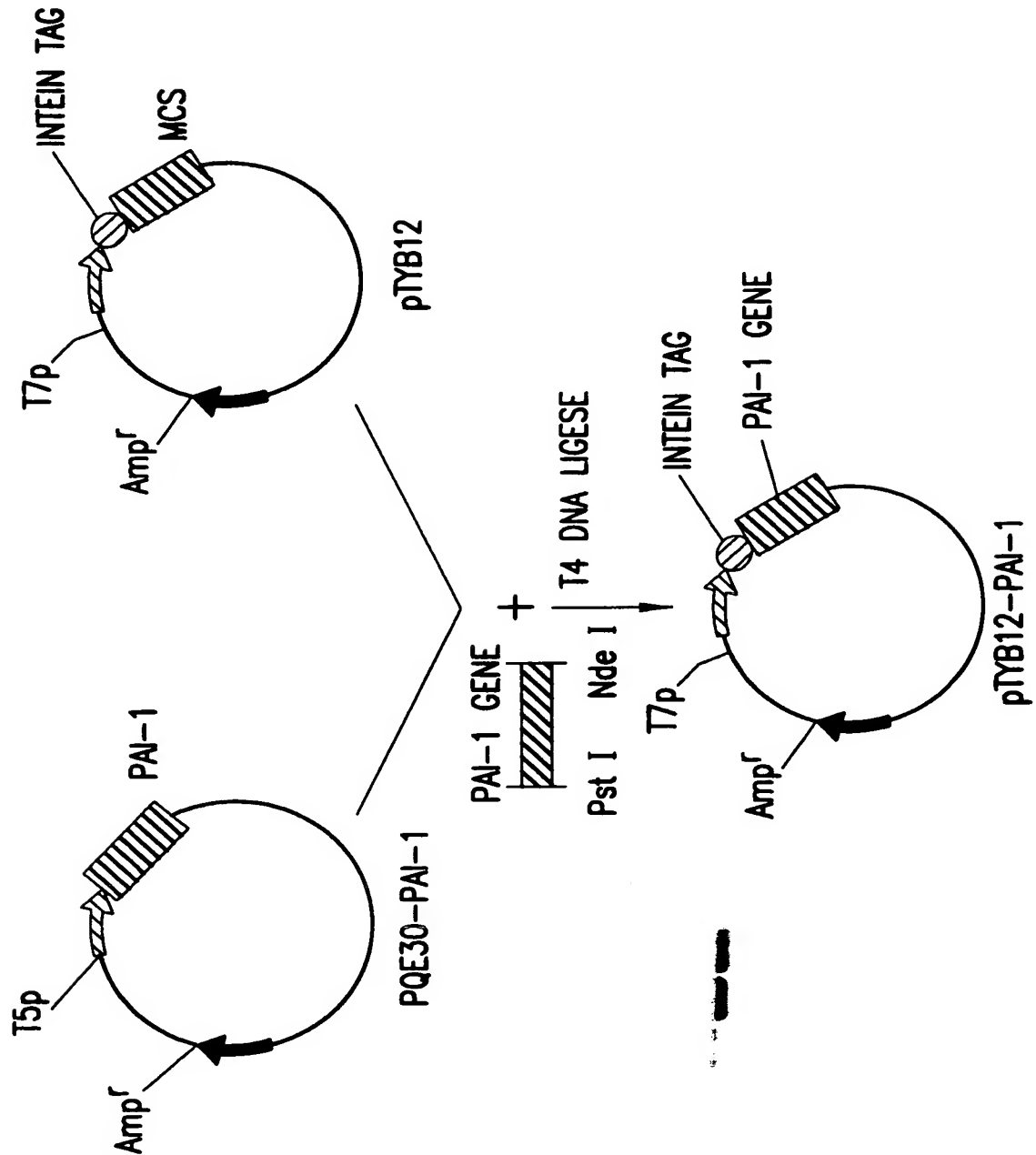


FIG.7

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FIG. 8A



FIG. 8B

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FIG. 9A



FIG. 9B

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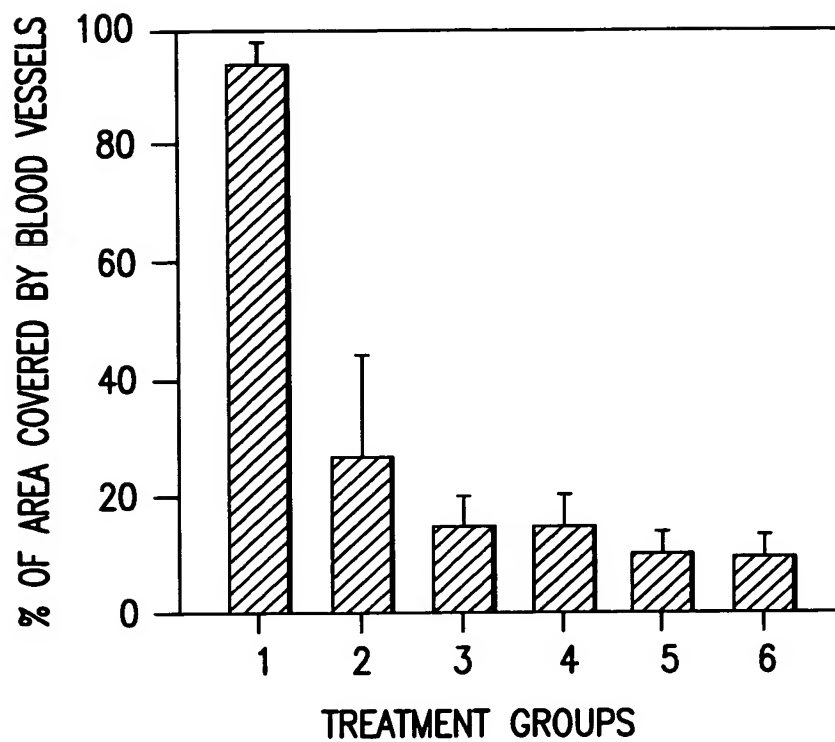


FIG.10

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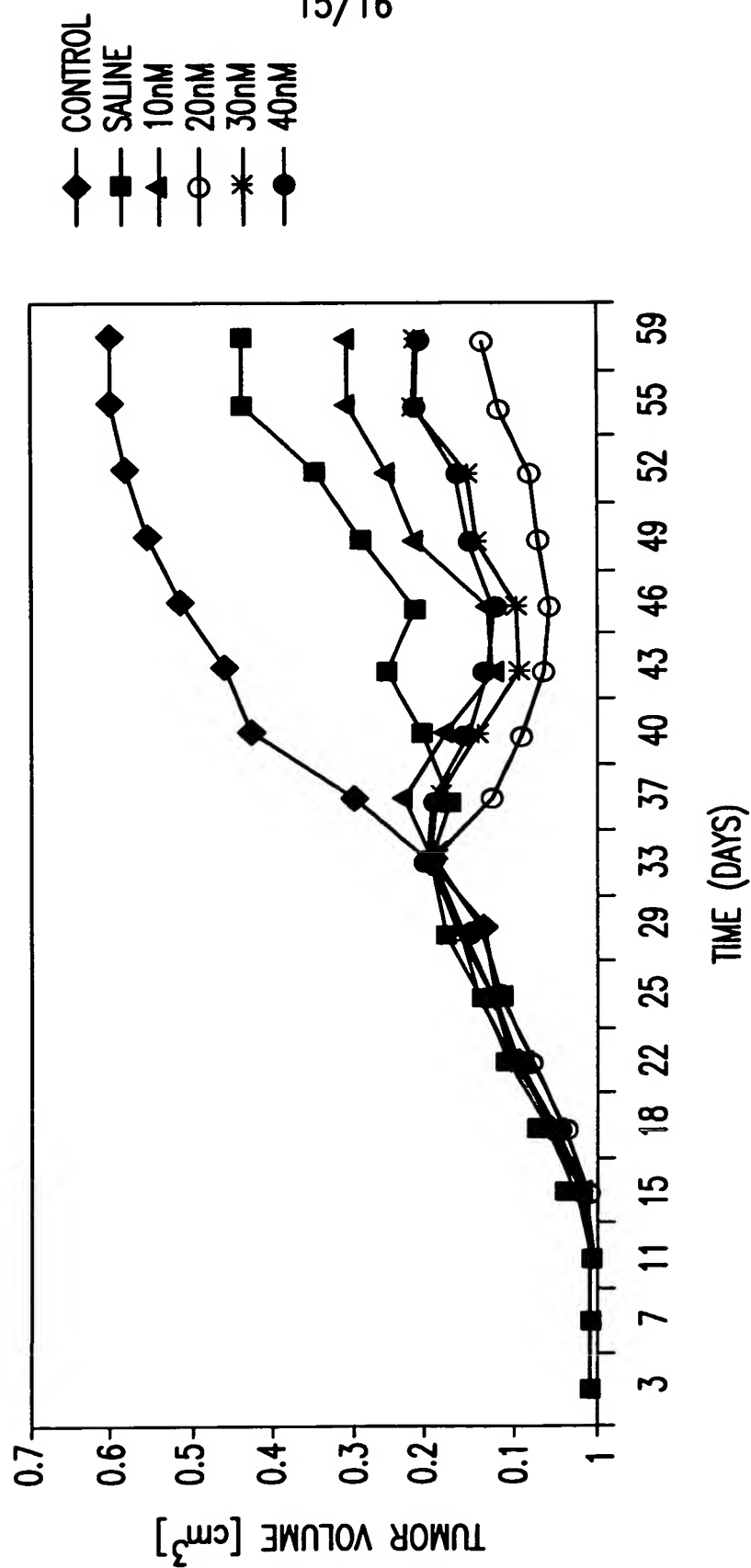


FIG.11

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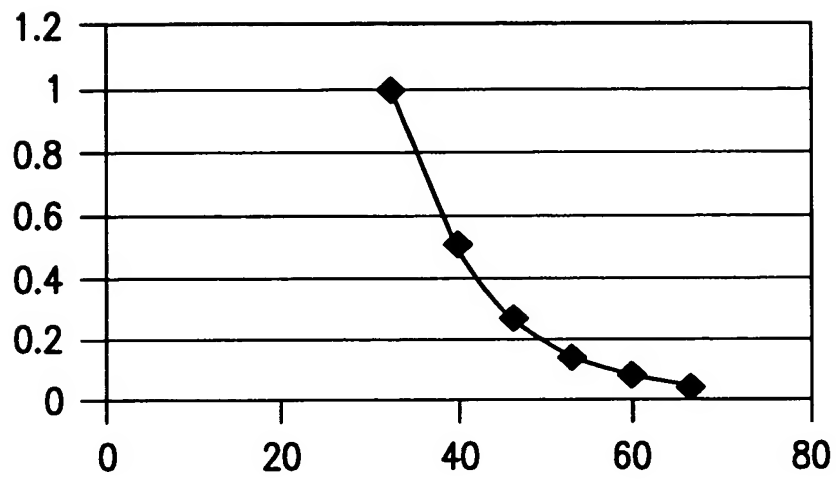


FIG.12